I enclose a file containing the nucleotide sequence of the PRE7(IAP) as is the provisional name we have selected for this element, which is involved in posttranscriptional regulation.

We have identified elements that have homology to PRE7(IAP) from the databases. The alignment of these elements is provided. None of these elements has been characterized functionally. Our work is the first that identified these sequences as potential posttranscriptional control elements. At present, PRE7(IAP) is the only one for which we have functional data.

In the aligned sequences, our functional PRE7(IAP) is called FNC3B. Only the "core" 231 nt element containing the functional element is shown.


```
FNC3B
GTGGGGTGCGAGGCTAAGCACTGCACAGAGGATAGCTTGCTGTTGGCATCCTGTGGAAGG
CACGTCTGATTGCATGAAGGTTCAGTGTCCTAGTTCCCTTCCCCCAGGAAAAACGACACG
GGAGCTGGCCAAGACCTCTCTGGGTGATGAGCCTAAGGGATGGTTTTGTGTAGGGCCCCT
ATGCTTGCACACTGGGGATCAGACCTCTACCTTCACCCATGAGGCTTGCTT
```


```
PRE7(IAP)

CTTTCGCCATGGTAGCATAGGCTTTTGCTGCAGTGGAGGCGGGACAATCTCCTCAGATTC
GGTTTGCCGCTCTAAAAGAAATTATGCTGCGTTATGCCGTGGGGTGCGAGGCTAAGCACT
GCACAGAGGATAGCTTGCTGTTGGCATCCTGTGGAAGGCACGTCTGATTGCATGAAGGTT
CAGTGTCCTAGTTCCCTTCCCCCAGGAAAAACGACACGGGAGCTGGCCAAGACCTCTCTG
GGTGATGAGCCTAAGGGATGGTTTTGTGTAGGGCCCCTATGCTTGCACACTGGGGATCAG
ACCTCTACCTTCACCCATGAGGCTTGCTTGCAGCAATTAAGATCTGGCCATAGGTTAATT
AACATCCTGGCCTTTTGATGCACCTGCCACAAG
```


the underlined sequences correspond to the aligned fragment FNC3B

The alignment of the sequences found in the database follows:

Exhibit I

```
FNC3B.seq        Begin:99 End:329
GB:X57268        Begin:1599 End:1841
GB:M10134        Begin:7308 End:7538
GB:X01172        Begin:2423 End:2668
GB:M12515        Begin:188 End:418
AE000664.seq       Begin:118019 End:118264
GB:M18252        Begin:3418 End:3662
GB:M18251        Begin:1630 End:1874
GB:S74315        Begin:3824 End:4068
GB:M10062        Begin:2711 End:2955
GB:E00593        Begin:2711 End:2955
E01116.gb_pat        Begin:2711 End:2955
GB:E00594        Begin:3537 End:3781
E01117.gb_pat        Begin:4388 End:4632
GB:X54077        Begin:2200 End:2444
GB:X04120        Begin:4477 End:4721
GB:X97915        Begin:839 End:1083
GB:M17551        Begin:6474 End:6721
GB:U58494        Begin:6192 End:6439
U70139.gcg       Begin:4321 End:4565
```

```
!!NA_MULTIPLE_ALIGNMENT 1.0
PileUp of: @CTE-setClg.list

 Symbol comparison table: GenRunData:pileupdna.cmp  CompCheck: 6876

                      GapWeight: 2
               GapLengthWeight: 1

 CTE-setClg.msf  MSF: 251  Type: N              10:03  Check: 7329 ..

 Name: FNC3B        Len:   251  Check: 6699  Weight:  1.00
 Name: X57268       Len:   251  Check: 7888  Weight:  1.00
 Name: M10134       Len:   251  Check: 8724  Weight:  1.00
 Name: X01172       Len:   251  Check: 3612  Weight:  1.00
 Name: M12515       Len:   251  Check:  112  Weight:  1.00
 Name: AE000664     Len:   251  Check: 4675  Weight:  1.00
 Name: M18252       Len:   251  Check: 1995  Weight:  1.00
 Name: M18251       Len:   251  Check: 2423  Weight:  1.00
 Name: S74315       Len:   251  Check: 1833  Weight:  1.00
 Name: M10062       Len:   251  Check: 1751  Weight:  1.00
 Name: E00593       Len:   251  Check: 1751  Weight:  1.00
 Name: E01116       Len:   251  Check: 1751  Weight:  1.00
 Name: E00594       Len:   251  Check: 1811  Weight:  1.00
 Name: E01117       Len:   251  Check: 1811  Weight:  1.00
 Name: X54077       Len:   251  Check: 2537  Weight:  1.00
 Name: X04120       Len:   251  Check: 2537  Weight:  1.00
 Name: X97915       Len:   251  Check: 3213  Weight:  1.00
 Name: M17551       Len:   251  Check: 5139  Weight:  1.00
 Name: U58494       Len:   251  Check: 5139  Weight:  1.00
 Name: U70139       Len:   251  Check: 1928  Weight:  1.00

//

          1
   FNC3B  GTGGGGTGCG AGGCTAAGC. ACTGCACAGA GGATAGCTT. ...GCTGT.T GG.CATCCTG T.GGAAGGCA CGTC
  X57268  GAGAGTTGTA AGACTAAGT. ACTGCACAGA GATTAGTCTA GAAGCTGT.T GGACAGTCTC T.GAGAGGCA TGTC
  M10134  AGGAGTTGCA AGGCTAAGC. ACTGCACAGG AGAGG.TCTG CGG..TATAA CGACTTTCTC CTGGGAGATA AGTC
  X01172  GAGAGTTGCA CGGCTAAGC. ACTGCAGTAG AAGGGCTCTG CGGCACATAT GAGCCTATTC TAGGGAGACA TGTC
  M12515  GAGAGTCG.A AGGCTAAGCA ACTGCAATGG AAAGGCTCTG CGGCATATAT GAGCCTATTC TAGGGAGACA TGTC
 AE000664 GAGAGTTGCA CGGCTAAGC. ACTGCAGTAG AAAGGCTCTG CGGCATATAT GAGCCTATTC TAGGGAGACA TGTC
  M18252  GAGAGTTGCA CGGCTAAGC. ACTGCAATGG AAAGGCTCTG CGGCATATAT GAGCCTATTC TAGGGAGACA TGTC
  M18251  GAGAGTTGCA AGGCTAAGC. ACTGCAATGG AAAGGCTCTG CGGCATATAT GAGCCTATTC TAGGGAGACA TGTC
  S74315  GAGAGTTGCA CGGCTAAGC. ACTGCAATGG AAAGGCTCTG CGGCATATAT GAGCCTATTC TAGGGAGACA TGTC
  M10062  GAGAGTTGCA AGGCTAAGC. ACTGCAATGG AAAGGCTCTG CGGCATATAT GAGCCTATTC TAGGGAAACA TGTC
  E00593  GAGAGTTGCA AGGCTAAGC. ACTGCAATGG AAAGGCTCTG CGGCATATAT GAGCCTATTC TAGGGAAACA TGTC
```

```
E01116    GAGAGTTGCA AGGCTAAGC. ACTGCAATGG AAAGGCTCTG CGGCATATAT GAGCCTATTC TAGGGAAACA TGTC.
E00594    GAGAGTTGCA AGGCTAAGC. ACTGCAATGG AAAGGCTCTG CGGCATATAT GAGCCTATTC TAGGGAGACA TGTC.
E01117    GAGAGTTGCA AGGCTAAGC. ACTGCAATGG AAAGGCTCTG CGGCATATAT GAGCCTATTC TAGGGAGACA TGTC.
X54077    GAGAGTTGCA AGGCTAAGC. ACTGCAATGG AAAGGCTCTG CGGCATATAT GAGCCTATTC TAGGGAGACA TGTC.
X04120    GAGAGTTGCA AGGCTAAGC. ACTGCAATGG AAAGGCTCTG CGGCATATAT GAGCCTATTC TAGGGAGACA TGTC.
X97915    GAGAGTTGCA AGGCTAAGC. ACTGCAATGG AAAGGCTCTG CGGCATATAT GTGCCTATTC TAGGGGGACA TGTC.
M17551    GAGAGTTGCA CGGCTAAGC. ACTGCAATGG AAAGGCTCTG CGGCATATAT GAGCCTATTC TAGGGAGACA TGTC.
U58494    GAGAGTTGCA CGGCTAAGC. ACTGCAATGG AAAGGCTCTG CGGCATATAT GAGCCTATTC TAGGGAGACA TGTC.
U70139    GAGAGTTGCA AGGCTAAGC. ACTGCAATGG AAAGGCTCTG CGGCATATAT GAGCCTATTC TAGGGNGACA TGTC.

          101
FNC3B     AGTTCCCTTC .CCCCAGGAA AAACGACACG GGAGCTGGCC AAGACC.TCT CTGGGTGA.. .....TGAGC CT.A
X57268    AGGGACCTTT .CCCCAGAAA AAAGGGCACA GGAGCAGGTC AGGGTT.ACT CTGGGTAAAG ATCTGTGGGC CT.G
M10134    GATCTCCTT. .CCCCCAGAA AAAAGACATC GGA.CTGGTC AGGACTTCCT CTGGGGATAA G......ACC CTGG
X01172    AGTGTCCTTC TCCCCAGGAA AAACGGCACG GGAGCAGGTC AGGGTT.GCT CTGGGTAAAA GCCTGTGAGC CT.A
M12515    AGTTCCCTTC .CCCCAGGCA AAACGACACG GGA.CAGGTC AGGGTT.GCT CTGGGTAAAA .CCTGTAAGC CT..
AE000664  AGTGTCCTTC TCTCCAGGCA AAACGACACG GGAGCAGGTC AGGGTT.GCT CTGGGTAAAA GCCTGTGAGC CT.A
M18252    AGTTCCCTTC .CCCCAGGCA AAACGACACG GGAGCAGGTC AGGGTT.GCT CTGGGTAAAA GCCTGTGAGC CT.A
M18251    AGTTCCCTTC .CCCCAGGCA AAACGACACG GGAGCAGGTC AGGGTT.GTT CTGGGTAAAA GCCTGTAAGC CT.A
S74315    AGTTCCCTTC .CCCCAGGCA AAACGACACG GGAGCAGGTC AGGGTT.GCT CTGGGTAAAA GCCTGTAAGC CT.A
M10062    AGTTCCCTTC .CCCCAGGCA AAACGACACG GGAGCAGGTC AGGGTT.GCT CTGGGTAAAA GCCTGTAAGC CT.A
E00593    AGTTCCCTTC .CCCCAGGCA AAACGACACG GGAGCAGGTC AGGGTT.GCT CTGGGTAAAA GCCTGTAAGC CT.A
E01116    AGTTCCCTTC .CCCCAGGCA AAACGACACG GGAGCAGGTC AGGGTT.GCT CTGGGTAAAA GCCTGTAAGC CT.A
E00594    AGTTCCCTTC .CCCCAGGCA AAACGACACG GGAGCAGGTC AGGGTT.GCT CTGGGTAAAA GCCTGTAAGC CT.A
E01117    AGTTCCCTTC .CCCCAGGCA AAACGACACG GGAGCAGGTC AGGGTT.GCT CTGGGTAAAA GCCTGTAAGC CT.A
X54077    AGTTCCCTTC .CCCCAGGCA AAACGACACG GGAGCAGGTC AGGGTT.GCT CTGGGTAAAA GCCTGTGAGC CT.A
X04120    AGTTCCCTTC .CCCCAGGCA AAACGACACG GGAGCAGGTC AGGGTT.GCT CTGGGTAAAA GCCTGTGAGC CT.A
X97915    AGTTCCCTTC .CCCCAGGCA AAACGACACG GGAGCAGGTC AGGGTT.GCT CTGGGTAAAA GCCTGTGAGC CT.G
M17551    AGTTGCCCT. TCCCCAGGCA AAACGACAC. GGAGCAGGTC AGGGTTGGCT CTGGGTAAAA GCCTGTGAGC CTC.A
U58494    AGTTGCCCT. TCCCCAGGCA AAACGACAC. GGAGCAGGTC AGGGTTGGCT CTGGGTAAAA GCCTGTGAGC CTC.A
U70139    AGTTCCCTTC .CCCCAGGCA AAACGACACG GGAGCAGGTC AGGGTT.GCT CTGGGTAAAA GCCTGTAAGC CT.A

          201                                                 251
FNC3B     TG.CTTGCAC ACTGGGGATC AGACCTCTAC CTTCACCCAT GAGGCTTGCT T
X57268    AC.ATGACAC ACTGGGGATC AGACCTCTAC CTCTACCCAC GGAGCTTGCT T
M10134    T...TTGCAC A.TGGGGATT TGACCTCTAT CTCCACTC.C AAAGTTGTGG G
X01172    T.ACCTGCAC ACTGGGGATT TGACCTCTAT CTCCACTCTC ATTAATATGG G
M12515    TTACCTACAC ACTGGG.... TGACCTCTAT CT.CACTCTC ATCAATATGG T
AE000664  T.ACCTACAC ACTGGGGATT TGACCTCTAT CTCCACTCTC ATTAGTTGGG T
M18252    T.ACCTACAC ACTGGGGATT TGACCTCTAT CTCCACTCTC ATTAATATGG G
M18251    T.ACCTACAC ACTGGGGATT TGACCTCTAT CCTCACTCTC ATTAATATGG G
S74315    T.ACCTACAC ACTGGGGATT TGACCTCTAT CTCCAGTCTC ATTAATATGG G
M10062    T.ACCTACAC ACTGGGGATT TGACCTCTAT CTCCACTCTC ATTAATATGG G
E00593    T.ACCTACAC ACTGGGGATT TGACCTCTAT CTCCACTCTC ATTAATATGG G
E01116    T.ACCTACAC ACTGGGGATT TGACCTCTAT CTCCACTCTC ATTAATATGG G
E00594    T.ACCTACAC ACTGGGGATT TGACCTCTAT CTCCACTCTC ATTAATATGG G
E01117    T.ACCTACAC ACTGGGGATT TGACCTCTAT CTCCACTCTC ATTAATATGG G
X54077    T.ACCTACAC ACTGGGGATT TGACCTCTAT CTCCACTCTC ATTAATATGG G
X04120    T.ACCTACAC ACTGGGGATT TGACCTCTAT CTCCACTCTC ATTAATATGG G
X97915    T.ACCTACAC ACTGGGGATT TGACCTCTAT CTCCACTCTC ATTAATATGG G
M17551    TGACCTACAC ACTGGGGATT TGACCTCTAT CTCCACTCTC ATTAATATGG G
U58494    TGACCTACAC ACTGGGGATT TGACCTCTAT CTCCACTCTC ATTAATATGG G
U70139    T.ACCTACAC ACTGGGGATT TGACCTCTAT CTCCACTCTC ATTAATATGG G
```

Plurality: 2.00 Threshold: 1 AveWeight 1.00 AveMatch 1.00 AvMisMatch 0.00

PRETTY of: CTE-setClg.msf(*)   10:04 ..